

vs.

```
Local similarity
Match: 19
Mismatch: -17
Indel start: -13
Indel extend: -7
```

Score: 8776 at (SEQ ID NO:38) [456..951] : (Jacobs et. al.) [1..481]

Arrow indicates polynucleotide encoding the C-terminal 15 amino acids of SEO ID NO:83.

[illegible]

TGA = STOP codon for SEQ ID NO:83

512 CAACGGGATTCTTTTGCTTTGAAAAATGTTGCAGTCCACCTGTCCAACCTGATCTTCCGGA  
50 CAACGGGATTCTTTTGCTTTGAAAAATGTTGCAGTCCACCTGTCCAACCTGATCTTCCGGA

572 CATTTGACTTGGTTCTGGTTATCCACCATCTCTTGCCTTCTTGGGTTCTTGGCTGCT  
|||  
110 CATTTGACTTGGTTCTGGTTATCCACCATCTCTTGCCTTCTTGGGTTCTTGGCTGCT

632 TGGTCAATCTCCAAGCTGGCCACTATCTAGCTATGACCACGTTGCTCCTGGAGATGAGCA  
|||  
170 TGGTCAATCTCCAAGCTGGCCACTATCTAGCTATGACCACGTTGCTCCTGGAGATGAGCA

692 CGCCCTTTACCTGCGTTTCCTGGATGCTCTTAAAGGCGGGCTGGTCCGAGTCTCTGTTT  
|||  
230 CGCCCTTTACCTGCGTTTCCTGGATGCTCTTAAAGGCGGGCTGGTCCGAGTCTCTGTTT

752 GGAAGCTCAACCAGTGGCTGATGATTCACATGTTTCACTGCCGCATGGTTCTAACCTACC  
|||  
290 GGAAGCTCAACCAGTGGCTGATGATTCACATGTTTCACTGCCGCATGGTTCTAACCTACC

812 ACATGTGGTGGGTGTGTTTCTGGCACTGGGACGGCCTGGTCAGCAGCCTGTATCTGCCTC  
|||  
350 ACATGTGGTGGGTGTGTTTCTGGCACTGGGACGGCCTGGTCAGCAGCCTGTATCTGCCTC

872 ATTTGACACTGTTCC<sup>TT</sup>GTCTGGACTGGCTCTGCTTACGCTAATCATTAATCCATATTGGA  
 |||||  
 410 ATTTGACACTGTTCC<sup>TT</sup>GTCTGGACTGGCTCTGCTTACGCTAATCATTAATCCATATTGGA

932 CCCATAAGAAGACTCAGCAG  
||| ||||| | ||  
470 CCC-----AGACTC-G-AG

Percent Identity: 95.0  
Percent Similarity: 95.0